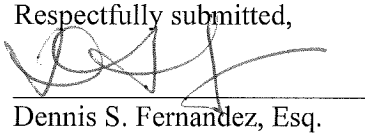
REMARKS

To overcome Examiner 35.USC.102e rejection of claims 1, 27 and 28 over Holden; and 35.USC.103a rejection of claims 10-12-21 and 23-26 over Holden, claims 2-4, 6-9 and 22 over Holden in view of Asch, and claim 5 over Holden and O'Flaherty, applicant amends independent claims herein to distinguish cited references patentably by specifying among other things the limitation: "wherein the bioinformatic value is automatically determined using a non-discriminatory sample sequence segment or index for predictably analyzing the voluntarily-selected portion of personal genetic nucleotide and related protein folding structure profile to enable transactional evaluation predictably according to actual user protein folding structure function."

Applicant's invention as clarified further herein would be unobvious to a person of ordinary skill in the art at the time the invention was made, significantly because conventional approaches, such as Holden, merely consider genetic markers, but not actual user protein folding structure. While there are a very large number of possible genetic markers, it is not predictable which (if any) of such genetic markers would be necessarily expressed into particular protein folding structures; and thus applicant respectfully submits that it would be unobvious for a routineer to try with any reasonable expectation of success to enable predictive transactional evaluation that is necessarily based on actual user protein folding structure, as claimed herein.

Respectfully submitted,



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